This listing of claims will replace all prior versions, and listings, of claims in the application.

Please cancel claims 16-54, and 60-62, without prejudice.

Listing of claims:

1-54. (Canceled).

55. (Previously presented) A method for determining whether a gene contributes to Attention Deficit Hyperactivity Disorder (ADHD), comprising:

(a) identifying a group of subjects with ADHD;

(b) selecting a group of candidate genes;

(c) identifying a polymorphism associated with each candidate gene;

(d) creating a scale corresponding to severity of ADHD in each subject;

(e) assigning a gene score to each candidate gene according to relative effect of the subject's candidate gene genotype to phenotype;

(f) determining additive variance (r^2) of said candidate genes using multivariate regression analysis and backward elimination of nonsignificant candidate genes; and

(g) calculating statistical significance of each candidate gene, wherein statistical significance indicates that said gene contributes to ADHD.

56. (Previously presented) The method of claim 55, wherein said group of candidate genes comprises norepinephrine genes.

57. (Previously presented) The method of claim 55, wherein said group of candidate genes comprises neurotransmitter genes.

58. (Previously presented) The method of claim 55, wherein said group of candidate genes comprises opioid genes.

59. (Previously presented) The method of claim 55, wherein said group of candidate genes comprises serotonin genes.

60-62. (Canceled).

63. (Previously presented) A method for treating a subject at risk for ADHD, comprising administering a drug known to regulate a gene determined by the method of claim 55 to contribute to ADHD.

64. (Previously presented) A method for determining whether a subject is at risk for ADHD comprising determining if said subject comprises one or more non-wild type alleles of a gene determined by the method of claim 55 to contribute to ADHD.

65.(New) The method of claim 64, wherein said non-wild type allele is selected from the group consisting of *TPH* SNP A 779C, *ADRA2A* SNP promoter region *Msp*I, *ADRA2C* dinucleotide repeat, *PNMT* SNP G-148A, *NET* SNP A1970G *Mnl*I, *COMT* SNP val 158 met G1947A *Nla*III, *CHRNA4*, *ADOA2A* SNP C108T *Rsa*l, *NOS3*, and *NAT1* T1088A.

66. (New) The method of claim 65, wherein an increase in the number of said non-wild type alleles indicates an increased risk of ADHD.

67. (New) The method of claim 66, wherein an increase in the number of said non-wild type alleles indicates an increase in the severity of ADHD.